Amendments to the Specification:

Please replace the paragraph beginning at page 15, line 25, with the following amended paragraph:

The "percent identity" of two amino acid sequences or of two nucleic acids is determined using the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci.* USA 87:2264-2268, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci.* USA 90:5873-5877. Such an algorithm is incorporated into the Blastall (BLASTP, BLASTX, TBLASTN, TBLASTX) or Bl2seq programs (version 2.x and later) of Altschul et al. (1990). *J. Mol. Biol.* 215:403-10. Bl2seq performs a comparison between the subject sequence and a target sequence using either the BLASTN (used to compare nucleic acid sequences) or BLASTP (used to compare amino acid sequences) algorithm. Typically, the default parameters of a BLOSUM62 scoring matrix, gap existence cost of 11 and extension cost of 1, a word size of 3, an expect value of 10, a per residue cost of 1 and a lambda ratio of 0.85 are used when performing amino acid sequence alignments. The output file contains aligned regions of homology between the target sequence and the subject sequence. Once aligned, a length is determined by counting the number of consecutive nucleotides or amino acid residues (*i.e.*, excluding gaps) from the target sequence that align with sequence from the subject sequence starting with any matched position and ending with any other matched position. A matched position is any position where an identical nucleotide or amino acid residue is present in both the target and subject sequence. Gaps of one or more residues can be inserted into a target or subject sequence to maximize sequence alignments between structurally conserved domains (*e.g.*, α-helices[[,]] and β-sheets, and loops).

Please replace the paragraph beginning at page 23, line 21, with the following amended paragraph:

The nematode proteins and plant homologs are all presumably localized in the cytosol as in the case of the wheat PEAMT as they lack secretion leaders (analyzed by methods available on the Internet at cbs.dtu.dk/services/Target P) ~~(http://www.cbs.dtu.dk/services/TargetP/)~~ or transmembrane regions (analyzed by available on the Internet at cbs.dtu.dk/services.TMHMM).

Please replace the paragraph beginning at page 33, line 9, with the following amended paragraph:

The similarity between *A. suum, H. contortus, M. incognita, M. javanica* and *S. stercoralis* PEAMT-like sequences and other sequences were also investigated by comparison to sequence databases using BLASTP analysis against nr (a non-redundant protein sequence database available at www.ncbi.nlm.nih.gov) and TBLASTN analysis against dbest (an EST sequence database available at [[www.]]ncbi.nlm.nih.gov; top 500 hits; E = 1e-4). The "Expect (E) value" is the number of sequences that are predicted to align by chance to the query sequence with a score S or greater given the size of the database queried. This analysis was used to determine the potential number of plant and vertebrate homologs for each of the nematode PEAMT-like polypeptides described above. *A. suum* (SEQ ID NO: 1 and 5), *H. contortus* (SEQ ID NO:2), *M. incognita* (SEQ ID NO:3), *M. javanica* (SEQ ID NO: 6), *S. stercoralis* (SEQ ID NO:4) and *C. elegans* (SEQ ID NO:19, 20 and 21) PEAMT-like sequences had no high scoring vertebrate hits in **nr** or **dbest** having sufficient sequence similarity to meet the threshold E value of 1e-4 (this E value approximately corresponds to a threshold for removing sequences having a sequence identity of less than about 25% over approximately 100 amino acids). Accordingly, the *A. suum, H. contortus, M. incognita, M. javanica* and *S. stercoralis* PEAMT-like enzymes of this invention do not appear to share significant sequence similarity with common vertebrate methyltransferase enzymes such as the *Homo sapiens* gi|13345056|gb|AAK19172.1|[13345056])

or the *Rattus norvegicus* (gi|310195|gb|AAA03154.1|[310195]) phosphatidylethanolamine n-methyltransferase.

Please replace the paragraph beginning at page 41, line 19, with the following amended paragraph:

Database Identification. A nematode phosphoethanolamine n-methyltransferase-like sequence can be identified from a sequence database, e.g., a protein or nucleic acid database using a sequence disclosed herein as a query. Sequence comparison programs can be used to compare and analyze the nucleotide or amino acid sequences. One such software package is the BLAST suite of programs from the National Center for Biotechnology Institute (NCBI; Altschul et al. (1997) *Nucl. Acids Research* 25:3389-3402). A phosphoethanolamine n-methyltransferase -like sequence of the invention can be used to query a sequence database, such as nr, dbest (expressed sequence tag (EST) sequences), and htgs (high-throughput genome sequences), using a computer-based search, e.g., FASTA, BLAST, or PSI-BLAST search. Homologous sequences in other species (e.g., plants and animals) can be detected in a PSI-BLAST search of a database such as nr (E value = 10, H value = 1e-2, using, for example, four iterations; available at [[www.]]ncbi.nlm.nih.gov). Sequences so obtained can be used to construct a multiple alignment, e.g., a ClustalX alignment, and/or to build a phylogenetic tree, e.g., in ClustalX using the Neighbor-Joining method (Saitou et al. (1987) *Mol. Biol. Evol.* 4:406-425) and bootstrapping (1000 replicates; Felsenstein (1985) *Evolution* 39:783-791). Distances may be corrected for the occurrence of multiple substitutions [$D_{corr} = -\ln(1-D-D^2/5)$ where D is the fraction of amino acid differences between two sequences] (Kimura (1983) *The Neutral Theory of Molecular Evolution*, Cambridge University Press).